

Amendments to the Specification

Please replace the paragraph at page 1, beginning with line 10 with the following:

This application claims the benefit of U.S. Provisional Application No. 60/135,391 filed May 21, 1999, U.S. Provisional Application No. 60/092,936 filed July, 15 1998, U.S. Application No. 09/352,168 filed July 12, 1999, now issued U.S. Patent Number 6,211,434 and is a Continuation of U.S. Application No. 09/352,159 filed July 12, 1999, now issued U.S. Patent Number 6,211,435 all of which are hereby incorporated by reference.

Q1 Please replace the paragraph at page 59, beginning at line 15 with the following: *7*

The amine oxidase domain of trAPAO contains several key features shared by this class of enzymes, including an amino-terminal dinucleotide (ADP) binding region characterized by a beta-alpha-beta stretch containing three invariant glycines (G -X-G-X-X-G) in the beta-alpha turn. In trAPAO, this sequence is (DVVVVGAGLSG) (SEQ ID NO: 54). This region is involved in FAD binding. Absent are several features unique to the mammalian amine oxidases, including several essential cysteine residues (Wu *et al.*, *Mol Pharm* 43:888 (1993)), one of which (Cys-406 of MAO-A) is involved in covalent binding of FAD, and a carboxy-terminal extension that has been demonstrated to be involved in transporting to and anchoring the MAO in the outer mitochondrial membrane. The *Aspergillus* enzyme MAO-N has been demonstrated to contain non-covalent FAD, and also lacks the conserved cysteine. Therefore it is possible that the APAO enzyme has a non-covalent FAD. The *Aspergillus* MAO-N has a carboxy-terminal tripeptide Ala-Arg-Leu that is involved in peroxisomal targeting and localization; this sequence is absent from *Exophiala* MAO.

Q2 Please replace the paragraph at page 68, beginning at line 25 with the following: *7*

Preliminary sequence results were entered into GCG, and nucleotide and protein alignments were done in a pileup using a software program called Genedoc for shading and homology comparisons (Nicholas, *et al.*, *EMBNEW.NEWS* 4:14 (1997; or at the Internet site <http://www.cris.com/~Ketchup/genedoc.shtml>) www.cris.com/~Ketchup/genedoc.shtml). The

first APAO (SEQ ID NO: 22) sequences were included for comparison. Comparing the reference sequence SEQ ID NO: 22 to the other homologs sequence identities range from 96 to 99% (identities are lower since APAO introns were not included). Homologies are slightly higher comparing *Exophiala* genes sequences. At the amino acid sequence level the comparison of the reference sequence (SEQ ID NO: 23) to the other homologs yielded sequence identities of approximately 97%.
